CLEAN CLAIM SET

14.(Twice amended) The method according to claim 18, wherein said epitope is modified by:

(a) substituting the amino acid sequence of the epitope with an analogous sequence from a human homolog to the protein of interest;

(b) substituting the amino acid sequence of the epitope with an analogous sequence from a non-human homolog to the protein of interest; or

(c) substituting the amino acid sequence of the epitope with a sequence which substantially mimics the major tertiary structure attributes of the epitope.

17. A method for determining a T-cell epitope of a peptide comprising the steps of:

(a) obtaining from a single human blood source a solution of dendritic cells and a solution of naïve CD4+ and/or CD8+ T-cells;

(b) promoting differentiation in said solution of dendritic cells;

(c) combining said solution of differentiated dendritic cells and said naïve CD4+ and/or CD8+ T-cells with the peptide, said peptide comprising said T-cell epitope; and

(d) measuring proliferation of said T-cells in said step (c).

18. A method of reducing the allergenicity of a protein comprising the steps of:

(a) identifying a T-cell epitope in said protein by

(i) contacting an adherent monocyte-derived dendritic cell with a peptide comprising said T-cell epitope; and

(ii) contacting said dendritic cell and peptide to a naïve T-cell whereby said T-cell proliferates in response to said peptide; and

(b) modifying said protein to neutralize said T-cell epitope such that the modified protein induces less than or substantially equal the baseline proliferation of said naïve T-cells.

19. The method according to claim 18, wherein the protein is a protease.

20. A method for reducing the allergenicity of a microbial subtilisin comprising the steps of:

(a) determining a T-cell epitope of said subtilisin comprising (i) obtaining from a single human blood source a solution of dendritic cells and a solution of naïve CD4+ and/or CD8+ T-cells; (ii) promoting differentiation in said solution of dendritic cells; (iii) combining said solution of differentiated dendritic cells and said naïve CD4+ and/or CD8+ T-cells with peptide fragments of said subtilisin, wherein one or more peptide fragments comprise the T-cell epitope of the subtilisin; and (iv) measuring proliferation of said T-cells in said step (iii); and
(b) modifying the peptide which includes the T-cell epitope to neutralize said epitope.

21. The method according to claim 20, wherein the microbial subtilisin is derived from a *Bacillus*.

22. The method according to claim 21, wherein the *Bacillus* is selected from the group consisting of *B. lentus*, *B. subtilisin*, *B. amyloliquefaciens* and *B. licheniformis*.

23. The method according to claim 20, wherein said epitope of the protein is modified by: (a) substituting the amino acid sequence of the epitope with an analogous sequence from a human homolog to the protein of interest; (b) substituting the amino acid sequence of the epitope with an analogous sequence from a non-human homolog to the protein of interest; or (c) substituting the amino acid sequence of the epitope with a sequence which substantially mimics the major tertiary structure attributes of the epitope

24. The method according to claim 14, wherein the protein is a protease.

25. The method according to claim 24, wherein the protease is a subtilisin.

26. The method according to claim 14, wherein said epitope is modified by substituting the amino acid sequence of the epitope with an analogous sequence from a human homolog to the protein of interest.

27. The method according to claim 14, wherein said epitope is modified by substituting the amino acid sequence of the epitope with an analogous sequence from a non-human homolog to the protein of interest.

28. The method according to claim 14, wherein said epitope is modified by substituting the amino acid sequence of the epitope with a sequence which substantially mimics the major tertiary structure attributes of the epitope.